

GenCore version 5.1.6
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OM protein - protein search, using SW model

Run on: July 27, 2005, 17:56:17 ; Search time 165 Seconds
(without alignments)
147.672 Million cell updates/sec

Title: US-09-981-845-11
Perfect score: 333
Sequence: 1 RSRATEVFTPVFTPVDYD.....AGGPAGPAGPAGPAGPAGPA 63

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04:
1: geneseqD1980s:
2: geneseqD1990s:
3: geneseqD2000s:
4: geneseqD2001s:
5: geneseqD2002s:
6: geneseqD2003abs:
7: geneseqD2003bbs:
8: geneseqD2004s:
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB	ID	Description
1	333	100.0	63	5	ABB76407		Abb76407 Osteopont
2	236	70.9	87	5	AAE18619		Abb18619 Biophys
3	207	62.2	40	5	ABB76406		Abb76406 Osteopont
4	201	60.4	40	5	ABB76410		Abb76410 Osteopont
5	200	60.1	40	5	ABB76404		Abb76404 Osteopont
6	181	54.4	49	5	ABB76405		Abb76405 Osteopont
7	181	54.4	192	5	ABG79674		Abb79674 Tumour in
8	181	54.4	218	8	ADS12215		Abb12215 Human the
9	181	54.4	243	8	ADJ67551		Adj67551 Human ora
10	181	54.4	243	8	ADJ67676		Adj67676 Human ora
11	181	54.4	273	7	AAO30815		Aao30815 Human cel
12	181	54.4	273	7	ADM47287		Adm47287 Osteopont
13	181	54.4	278	7	ADM47287		Adm47287 Osteopont
14	181	54.4	279	8	AAR30701		Aar30701 Isoform Q
15	181	54.4	282	2	AAR30704		Aar30704 Human the
16	181	54.4	286	6	ABP58125		Abp58125 Human ost
17	181	54.4	287	5	ABG96388		Abb96388 Human ora
18	181	54.4	287	6	ABR47551		Ab47551 Breast ca
19	181	54.4	287	6	ABR92133		Abb92133 Human cel
20	181	54.4	287	6	ADB7483		Adb7483 Prostate
21	181	54.4	287	6	ADQ88475		Adq88475 Human OPN
22	181	54.4	287	8	ADM47215		Adm47215 Osteopont
23	181	54.4	296	2	AAR30700		Aar30700 Human uro
24	181	54.4	299	6	ABP58124		Abp58124 Human ost

ALIGNMENTS

RESULT 1	
ID	ABB76407 standard; protein; 63 AA.
XX	
AC	ABB76407;
XX	
DT	27-AUG-2002 (first entry)
XX	
DE	Osteopontin-derived peptide.
XX	
KW	Osteopontin; osteopathic; bone; tissue formation; antiinflammatory; cell differentiation.
XX	
OS	Homo sapiens.
XX	
PN	WO0022940-A2.
XX	
PD	25-APR-2002.
XX	
PF	18-OCT-2001; 2001WO-US032457.
XX	
PR	18-OCT-2001; 2000US-0241245P.
XX	
PR	05-OCT-2001; 2001US-0327273P.
XX	
(CHIL-)	CHILDRENS MEDICAL CBNT.
XX	
PI	Askar S, Salcedo J;
XX	
DR	WPT; 2002-479661/51.
XX	
PT	Osteopontin derived peptides useful in implants e.g. dental screws or fixtures, and orthopedic joints.
PT	
PT	fixtures, and orthopedic joints.
XX	
CC	Claim 1; Page 8; 64pp; English.
XX	
CC	The present sequence is an osteopontin-derived peptide, which regulates cell development and binds to an integrin on a cell surface. The
CC	rate of osteointegration and the percentage of bone apposition. The
CC	implant includes osteopontin, an active fragment of osteopontin or an osteopontin-derived peptide such as the present claimed peptide. Claimed peptides of the invention (see ABB76403-11) bind to various cell types and play important roles in cellular differentiation, and/or motility. These cells include osteoprogenitor cells, tumour cells, macrophages, perosteal cells, endothelial cells, epithelial cells, eosinophils, stem cells, limited potential precursor cells, precursor cells, committed precursor cells, and differentiated cells. The peptides are also active as antiinflammatory agents. Antibodies provide a

CC mechanism to abolish or attenuate the activities of the claimed peptides.
 CC the implant can be used in an osteopontin containing cell recruitment
 CC system, to induce new tissue formation in a subject, and to promote cell
 CC differentiation (all claimed). The implants include surgical implants
 CC such as dental screws, jaw modifications, orthopaedic implants, face
 CC reconstruction implants, orthopaedic implants e.g. orthopaedic screws,
 CC rods or joints such as hip or knee replacement implants
 XX Sequence 40 AA;

CC rods or joints such as hip or knee replacement implants
 XX Sequence 40 AA;

Query Match 60.4%; Score 201; DB 5; Length 40;
 Best Local Similarity 97.5%; Pred. No. 2.6e-15;
 Matches 39; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Seq 1 RSRATEVFTPVVPTVDTYDGRGDSVYGRRSKSKKKFRRP 40
 1 RSRATEVFTPVVPTVDTYDGRGDSVYGRRSKSKKKFRRP 40

Query Match 62.2%; Score 207; DB 5; Length 40;
 Best Local Similarity 100.0%; Pred. No. 5.6e-16;
 Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 RSRATEVFTPVVPTVDTYDGRGDSVYGRRSKSKKKFRRP 40
 1 RSRATEVFTPVVPTVDTYDGRGDSVYGRRSKSKKKFRRP 40

RESULT 5

ABB76404
 ID ABB76404 standard; protein; 40 AA.
 XX
 AC ABB76404;
 XX
 DT 27-AUG-2002 (first entry)
 XX
 DE Osteopontin-derived peptide OC-1016.
 XX
 KW Osteopontin; osteopathic; bone; tissue formation; antiinflammatory;
 KW cell differentiation.
 XX
 OS Homo sapiens.
 XX
 PN WO20022940-A2.
 XX
 PD 25-APR-2002.

ABB76410
 ID ABB76410 standard; protein; 40 AA.
 XX
 AC ABB76410;
 XX
 DT 27-AUG-2002 (first entry)
 XX
 DE Osteopontin-derived peptide.
 KW Osteopontin; osteopathic; bone; tissue formation; antiinflammatory;
 KW cell differentiation.
 XX
 OS Homo sapiens.
 XX
 PN WO20022940-A2.
 XX
 PD 25-APR-2002.

ABB76410
 ID ABB76410 standard; protein; 40 AA.
 XX
 AC ABB76410;
 XX
 DT 27-AUG-2002 (first entry)
 XX
 DE Osteopontin-derived peptide.
 KW Osteopontin; osteopathic; bone; tissue formation; antiinflammatory;
 KW cell differentiation.
 XX
 OS Homo sapiens.
 XX
 PN WO20022940-A2.
 XX
 PD 25-APR-2002.

ABB76410
 ID ABB76410 standard; protein; 40 AA.
 XX
 AC ABB76410;
 XX
 DT 27-AUG-2002 (first entry)
 XX
 DE Osteopontin-derived peptide.
 KW Osteopontin; osteopathic; bone; tissue formation; antiinflammatory;
 KW cell differentiation.
 XX
 OS Homo sapiens.
 XX
 PN WO20022940-A2.
 XX
 PD 25-APR-2002.

ABB76410
 ID ABB76410 standard; protein; 40 AA.
 XX
 AC ABB76410;
 XX
 DT 27-AUG-2002 (first entry)
 XX
 DE Osteopontin-derived peptide.
 KW Osteopontin; osteopathic; bone; tissue formation; antiinflammatory;
 KW cell differentiation.
 XX
 OS Homo sapiens.
 XX
 PN WO20022940-A2.
 XX
 PD 25-APR-2002.

ABB76410
 ID ABB76410 standard; protein; 40 AA.
 XX
 AC ABB76410;
 XX
 DT 27-AUG-2002 (first entry)
 XX
 DE Osteopontin-derived peptide.
 KW Osteopontin; osteopathic; bone; tissue formation; antiinflammatory;
 KW cell differentiation.
 XX
 OS Homo sapiens.
 XX
 PN WO20022940-A2.
 XX
 PD 25-APR-2002.

ABB76410
 ID ABB76410 standard; protein; 40 AA.
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 AC ABB76410;
 XX
 DT 27-AUG-2002 (first entry)
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 DE Osteopontin-derived peptide.
 KW Osteopontin; osteopathic; bone; tissue formation; antiinflammatory;
 KW cell differentiation.
 XX
 OS Homo sapiens.
 XX
 PN WO20022940-A2.
 XX
 PD 25-APR-2002.

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 ID ABB76410 standard; protein; 40 AA.
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 PD 25-APR-2002.

ABB76410
 ID ABB76410 standard; protein; 40 AA.
 XX
 AC ABB76410;
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 DT 27-AUG-2002 (first entry)
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 DE Osteopontin-derived peptide.
 KW Osteopontin; osteopathic; bone; tissue formation; antiinflammatory;
 KW cell differentiation.
 XX
 OS Homo sapiens.
 XX
 PN WO20022940-A2.
 XX
 PD 25-APR-2002.

ABB76410
 ID ABB76410 standard; protein; 40 AA.
 XX
 AC ABB76410;
 XX
 DT 27-AUG-2002 (first entry)
 XX
 DE Osteopontin-derived peptide.
 KW Osteopontin; osteopathic; bone; tissue formation; antiinflammatory;
 KW cell differentiation.
 XX
 OS Homo sapiens.
 XX
 PN WO20022940-A2.
 XX
 PD 25-APR-2002.

ABB76410
 ID ABB76410 standard; protein; 40 AA.
 XX
 AC ABB76410;
 XX
 DT 27-AUG-2002 (first entry)
 XX
 DE Osteopontin-derived peptide.
 KW Osteopontin; osteopathic; bone; tissue formation; antiinflammatory;
 KW cell differentiation.
 XX
 OS Homo sapiens.
 XX
 PN WO20022940-A2.
 XX
 PD 25-APR-2002.

ABB76410
 ID ABB76410 standard; protein; 40 AA.
 XX
 AC ABB76410;
 XX
 DT 27-AUG-2002 (first entry)
 XX
 DE Osteopontin-derived peptide.
 KW Osteopontin; osteopathic; bone; tissue formation; antiinflammatory;
 KW cell differentiation.
 XX
 OS Homo sapiens.
 XX
 PN WO20022940-A2.
 XX
 PD 25-APR-2002.

ABB76410
 ID ABB76410 standard; protein; 40 AA.
 XX
 AC ABB76410;
 XX
 DT 27-AUG-2002 (first entry)
 XX
 DE Osteopontin-derived peptide.
 KW Osteopontin; osteopathic; bone; tissue formation; antiinflammatory;
 KW cell differentiation.
 XX
 OS Homo sapiens.
 XX
 PN WO20022940-A2.
 XX
 PD 25-APR-2002.

ABB76410
 ID ABB76410 standard; protein; 40 AA.
 XX
 AC ABB76410;
 XX
 DT 27-AUG-2002 (first entry)
 XX
 DE Osteopontin-derived peptide.
 KW Osteopontin; osteopathic; bone; tissue formation; antiinflammatory;
 KW cell differentiation.
 XX
 OS Homo sapiens.
 XX
 PN WO20022940-A2.
 XX
 PD 25-APR-2002.

ABB76410
 ID ABB76410 standard; protein; 40 AA.
 XX
 AC ABB76410;
 XX
 DT 27-AUG-2002 (first entry)
 XX
 DE Osteopontin-derived peptide.
 KW Osteopontin; osteopathic; bone; tissue formation; antiinflammatory;
 KW cell differentiation.
 XX
 OS Homo sapiens.
 XX
 PN WO20022940-A2.
 XX
 PD 25-APR-2002.

ABB76410
 ID ABB76410 standard; protein; 40 AA.
 XX
 AC ABB76410;
 XX
 DT 27-AUG-2002 (first entry)
 XX
 DE Osteopontin-derived peptide.
 KW Osteopontin; osteopathic; bone; tissue formation; antiinflammatory;
 KW cell differentiation.
 XX
 OS Homo sapiens.
 XX
 PN WO20022940-A2.
 XX
 PD 25-APR-2002.

Query Match 60.1%; Score 200; DB 5; Length 40;

RESULT 8
 ABG79674
 ID ABG79674 Standard; protein; 192 AA.
 XX
 AC
 XX
 DT 15-NOV-2002 (first entry)
 XX
 DE Tumour involved gene (TIG) splice variant protein, NV-5.
 XX
 Human; splice variant; tumour-involved gene; TIG;
 pharmaceutical composition; cancer; diagnostic; tumour; gene therapy;
 endothelial cell; cell differentiation; cell proliferation; apoptosis;
 gene therapy.
 XX
 OS Homo sapiens.
 XX
 PN US2002086384-A1.
 PD 04-JUL-2002.
 XX
 PF 13-MAR-2001; 2001US-00805020.
 XX
 PR 14-MAR-2000; 2000IL-00135402.
 PR 16-MAY-2000; 2000IL-00136154.
 XX
 PA (LEVI/) LEVINE Z.
 PA (DAVI/) DAVID A.
 PA (ROMA/) ROMANO C.
 PA (BERN/) BERNSTEIN J.
 XX
 PR Levine Z, David A, Romano C, Bernstein J;
 XX
 DR WPI; 2002-635679/68.
 DR N-PSDB; ABS65204.
 XX
 PR Novel nucleic acid sequence, which is an alternative splicing variant of
 tumor involved genes, useful for detecting cancer, predisposition to
 cancer, for evaluating cancer state and in gene therapy for treating
 cancer.
 XX
 PS Claim 4; Page 70-71; 180pp; English.
 XX
 CC The invention discloses isolated human nucleic acid alternative splicing
 variants that are all tumor-involved genes (TIGs). The nucleic acids and
 polypeptides are useful for determining the level of a nucleic acid or
 polypeptide in a biological sample, for detecting a variant nucleic acid
 or polypeptide sequence in a biological sample, for determining the level
 of variant nucleic acid or polypeptide sequences in a biological sample
 and for determining the ratio between the level of variant sequence in a
 first biological sample and the level of the original sequence from which
 the variant has been varied by alternative splicing in a second
 biological sample and for raising antibodies. A pharmaceutical
 composition comprising a carrier and the nucleic acid, is useful for
 treating diseases (e.g. cancer) that can be ameliorated or cured by
 increasing or decreasing the level of the encoded protein. The nucleic
 acids are also useful for diagnostic purposes, especially for detecting
 cancer or a predisposition to cancer, for evaluating the state or
 aggressiveness of cancer disease, in basic research, for understanding
 the physiological functions of the original TIG, in targeting or
 developing pharmaceuticals, for distinguishing various stages in the life
 cycle of the same type of cells which may be helpful for the development
 of pharmaceuticals for various cancer stages in which cell cycle is non-
 normal, for determining mutations in tumour-involved gene and in gene
 therapy. The polypeptides are useful for identifying compounds capable of
 binding to the variant product and modulating its activity and for
 modulating endothelial differentiation and proliferation, as well as to
 modulate apoptosis either *ex vivo* or *in vivo*. The sequences presented in
 ABG796700-ABG79705 are the new variants (NV) 1-36 proteins of the TIGs
 disclosed
 XX Sequence 192 AA;

RESULT 9
 ABG79674
 ID ABG79674 Standard; protein; 218 AA.
 XX
 AC
 XX
 DT 16-DEC-2004 (first entry)
 XX
 DE Human therapeutic contig protein - SEQ ID 2452.
 XX
 KW antiinflammatory; neuroprotective; antianaemic; cyrostatic; vulnerary;
 KW inflammatory; haemopoiesis; immunity; neurodegenerative; stem cell;
 KW aplastic anaemia; cancer; wound healing; gene therapy.
 XX
 OS Homo sapiens.
 XX
 Key Location/Qualifiers
 FH Misc-difference 1. 218
 FT /label= Unknown, OTHER
 FT /note= "OTHER = In-frame STOP codon"
 XX
 WO2004080148-A2.
 XX
 PD 23-SEP-2004.
 XX
 PP 30-SEP-2003; 2003WO-US030720.
 XX
 PR 02-OCT-2002; 2002US-0416186P.
 XX
 PA (NUVE-) NUVELO INC.
 XX
 PI Tang YT, Asundi V, Ren F, Zhang J, Wehrman T, Wang Z, Ma Y;
 PI Wang D, Chen R, Zhao QA, Wang J, Ghosh M, Xue AJ, Weng G, Zhou P;
 XX
 WPI; 2004-668857/65.
 DR N-PSDB; ABS11617.
 XX
 CC The invention relates to a novel isolated polynucleotide and the encoded
 polypeptide. The molecules of the invention demonstrate antiinflammatory,
 neuroprotective, antianaemic, cyrostatic and vulnerary activities and may
 be useful in preparing a composition for diagnosing or
 treating inflammatory, neurodegenerative or stem cell disorders, e.g.,
 aplastic anemia or cancer for promoting wound healing.
 XX
 PS Example 2; SEQ ID NO 2452; 718pp; English.
 XX
 CC The invention relates to a novel isolated polynucleotide and the encoded
 polypeptide. The molecules of the invention demonstrate antiinflammatory,
 neuroprotective, antianaemic, cyrostatic and vulnerary activities and may
 be useful in preparing a composition for diagnosing or treating
 inflammatory, haemopoiesis, immune, neurodegenerative or stem cell
 disorders, such as aplastic anaemia or cancer, as well as for promoting
 wound healing. The molecules may also be utilised during gene therapy
 procedures. The current sequence is that of a human therapeutic contig
 protein of the invention.
 XX
 SQ Sequence 218 AA;

RESULT 10
 ABG79674
 ID ABG79674 Standard; protein; 40 AA.
 XX
 AC
 XX
 DT 142-ATEVFTPVVPTVDTGRGDSVYYGRRSKSKKFRRP 40
 XX
 DE 169-ATEVFTPVVPTVDTGRGDSVYYGRRSKSKKFRRP 204

RESULT 10	PN	WO2004013311-A2.	
ID ADJ67551	XX	XX	
standard; protein: 243 AA.	PD	12-FEB-2004.	
XX	XX	XX	
AC	PP	06-AUG-2003 ; 2003WO-US024669.	
XX	XX	XX	
DT 06-MAY-2004 (first entry)	PR	06-AUG-2002 ; 2002US-0401469P.	
XX	XX	XX	
DE Human ovarian specific polypeptide SEQ ID NO:265.	(DIAD-) DIADEXUS INC.	(DIAD-) DIADEXUS INC.	
XX	PA	PA	
XX	XX	XX	
human; ovarian; cytostatic; immunostimulant; vaccine; gene therapy;	Macina RA, Salceda S, Liu C, Sun Y, Turner LR;	Macina RA, Salceda S, Liu C, Sun Y, Turner LR;	
ovarian cancer; immune response; cancer.	XX	XX	
XX	DR	WPI; 2004-169331/16.	
OS Homo sapiens.	PS	XX	
XX	PS	XX	
PN WO2004013311-A2.	English.	XX	
XX	XX	XX	
PD 12-FEB-2004.	XX	XX	
XX	XX	XX	
PF 06-AUG-2003 ; 2003WO-US024669.	The invention relates to novel isolated ovarian specific nucleic acid molecules and the polypeptides encoded by them. A protein of the invention has cytostatic and immunostimulant activity. A nucleic acid of the invention may have a use as a vaccine, and in gene therapy. The nucleic acid molecule or polypeptide, antibody or kit is useful in identifying, diagnosing, monitoring, staging, imaging and treating ovarian cancer and non cancerous disease states in ovarian tissue and in inducing an immune response against the ovarian cancer cell. The sequences shown in ADJ67535-ADJ67682 represent ovarian specific polypeptides of the invention.	CC	
XX	XX	CC	
PR 06-AUG-2002 ; 2002US-0401469P.	CC	CC	
XX	XX	CC	
PA (DIAD-) DIADEXUS INC.	CC	CC	
XX	XX	CC	
PI Macina RA, Salceda S, Liu C, Sun Y, Turner LR;	CC	CC	
XX	XX	CC	
PT New ovarian specific nucleic acid, useful in identifying, diagnosing, monitoring, staging, imaging and treating ovarian cancer and non-cancerous disease states in ovarian tissue.	CC	CC	
XX	XX	CC	
PR 2004-169331/16.	CC	CC	
XX	XX	CC	
DR WPI; 2004-169331/16.	CC	CC	
XX	XX	CC	
PT New ovarian specific nucleic acid, useful in identifying, diagnosing, monitoring, staging, imaging and treating ovarian cancer and non-cancerous disease states in ovarian tissue.	CC	CC	
XX	XX	CC	
PS Claim 12; SEQ ID NO 265 ; 586pp; English.	XX	XX	
XX	XX	XX	
CC The invention relates to novel isolated ovarian specific nucleic acid molecules and the polypeptides encoded by them. A protein of the invention has cytostatic and immunostimulant activity. A nucleic acid of the invention may have a use as a vaccine, and in gene therapy. The nucleic acid molecule or polypeptide, antibody or kit is useful in identifying, diagnosing, monitoring, staging, imaging and treating ovarian cancer and non cancerous disease states in ovarian tissue and in inducing an immune response against the ovarian cancer cell. The sequences shown in ADJ67535-ADJ67682 represent ovarian specific polypeptides of the invention.	CC	CC	
XX	XX	CC	
XX	XX	CC	
Qy 5 ATEVFTPVYPPTVDTYDGRGDSVYYGRRSKSKKFRRP 40	RESULT 12	RESULT 12	
Db 71 ATEVFTPVYPPTVDTYDGRGDSVYYGRRSKSKKFRRP 106	AAO30815	AAO30815	
XX	ID AAO30815	ID AAO30815	
XX	standard; protein: 273 AA.	standard; protein: 273 AA.	
XX	XX	XX	
XX	AC	AC	
XX	AAO30815;	AAO30815;	
XX	XX	XX	
XX	DT 22-SEP-2003 (first entry)	DT 22-SEP-2003 (first entry)	
XX	DB Human cell adhesion and extracellular matrix protein (CADECm) -5.	DB Human cell adhesion and extracellular matrix protein (CADECm) -5.	
XX	XX	XX	
XX	KW Human; cell adhesion and extracellular matrix protein; immune disorder;	KW Human; cell adhesion and extracellular matrix protein; immune disorder;	
XX	XX	XX	
XX	OS Homo sapiens.	OS Homo sapiens.	
XX	XX	XX	
XX	PN WO2004047526-A2.	PN WO2004047526-A2.	
XX	XX	XX	
XX	PD 12-JUN-2003.	PD 12-JUN-2003.	
XX	PP 26-NOV-2002 ; 2002WO-US038437.	PP 26-NOV-2002 ; 2002WO-US038437.	
XX	XX	XX	
XX	PR 30-NOV-2001 ; 2001US-0334343P.	PR 30-NOV-2001 ; 2001US-0334343P.	
DT 06-MAY-2004 (first entry)	PR 07-DEC-2001 ; 2001US-0334278P.	DT 06-MAY-2004 (first entry)	PR 07-DEC-2001 ; 2001US-0334278P.
XX	XX	XX	
DE Human ovarian specific polypeptide SEQ ID NO:390.	PR 04-JAN-2002 ; 2002US-0345069P.	DE Human ovarian specific polypeptide SEQ ID NO:390.	PR 04-JAN-2002 ; 2002US-0345069P.
XX	XX	XX	
PR 25-JAN-2002 ; 2002US-0351552P.	PR 14-FEB-2002 ; 2002US-0357168P.	PR 25-JAN-2002 ; 2002US-0351552P.	PR 14-FEB-2002 ; 2002US-0357168P.
XX	XX	XX	
PR 29-MAR-2002 ; 2002US-0369128P.	PR 05-APP-2002 ; 2002US-0370802P.	PR 29-MAR-2002 ; 2002US-0369128P.	PR 05-APP-2002 ; 2002US-0370802P.
XX	XX	XX	
OS Homo sapiens.	PA (INCYT - INCYTE GENOMICS INC.	OS Homo sapiens.	PA (INCYT - INCYTE GENOMICS INC.
XX	XX	XX	

PI	Baugh MR, Becha SD, Bhatia U, Blake JJ, Borowsky ML, Burrill JD, Delegeane AM, Elliott VS, Gandhi AR, Gierzen KJ, Gorvad AE, Griffin JA, Ho A, Jin P, Kable AE, Lal PG, Lee EA, Lee S, Lee SY, Marquis JP, Lehr-Mason PM, Ramkumar J, Richardson TW, Sprague WN, Swarnakar A, Tang TY, Tran B, Tran UK, Chawla NK, Warren BA, Yue H, Zheng W;	XX	PR 21-NOV-2001; 2001US-0331768P.
PI	WPI: 2003-513695/48.	DR	PR 21-FEB-2002; 2002US-0359191P.
PI	Delegeane AM, Elliott VS,	DR	PR 21-FEB-2002; 2002US-0359191P.
PI	Gandhi AR,	DR	PR 28-FEB-2002; 2002US-0360933P.
PI	Griffin JA,	DR	PR 01-MAR-2002; 2002US-0360810P.
PI	Ho A,	DR	PR 01-MAR-2002; 2002US-036178P.
PI	Jin P,	DR	PR 05-MAR-2002; 2002US-0361748P.
PI	Kable AE,	DR	PR 12-MAR-2002; 2002US-0363429P.
PI	Lal PG,	DR	PR 12-MAR-2002; 2002US-0363633P.
PI	Lee EA,	DR	PR 12-APR-2002; 2002US-0372141P.
PT	Lee S,	DR	PR 16-APR-2002; 2002US-0372967P.
PT	Lee SY,	DR	PR 16-APR-2002; 2002US-037301P.
PT	Marquis JP,	DR	PR 16-APR-2002; 2002US-0373063P.
PT	Lehr-Mason PM,	DR	PR 17-APR-2002; 2002US-0373280P.
PT	Ramkumar J,	DR	PR 17-APR-2002; 2002US-0373287P.
PT	Richardson TW,	DR	PR 19-APR-2002; 2002US-0373881P.
PT	Sprague WN;	DR	PR 02-JUL-2002; 2002US-00187375.
XX	Swarnakar A,	XX	XX
XX	Tang TY,	XX	XX
PS	Tran B,	XX	XX
PS	Tran UK,	XX	XX
XX	Chawla NK,	XX	XX
XX	Warren BA,	XX	XX
XX	Yue H,	XX	XX
XX	Zheng W;	XX	XX
DR	DR-PSDB;	DR	PR (CURA-) CURAGEN CORP.
DR	AAL62017.	XX	XX
XX	New human cell adhesion and extracellular matrix proteins (CADECIM) polypeptide, useful for preparing a composition for treating a disease associated with decreased expression or overexpression of CADECIM e.g., cancer.	XX	Li L, Shenoy SG, Paturrajan M, Ellerman K, Gorman L, Zhong M; Catterton S, Spytek KA, Miller CE, Edinger SR, Hjalti T, Gerlach VL; Shimkets RA, Taupier RJ, Anderson DW, Guo X, Baumgartner JC; Padigaru M, Payman JA, Smithson G, Casman SJ, Voss EZ, Boldog FL; Pena CEA, Chapoval A, Rastelli L, Kekuda R, Vernet CRM.
XX	Claim 1; Page 277; 374pp; English.	XX	WPI: 2003-812538/76.
XX	The invention relates to human cell adhesion and extracellular matrix proteins (CADECIM) and nucleic acid molecules encoding such proteins.	XX	DR N-PSDB; ADM47286.
CC	CADECIM proteins are useful for preparing a composition for diagnosing or treating disease or condition associated with decreased expression or overexpression of functional CADECIM e.g., immune disorders or cancer. The invention is also useful in gene therapy. The present sequence is human CADECIM protein	CC	CC The novel polypeptide comprises a sequence comprising 109-1671 amino acids, or its mature form; a sequence that is at least 95% identical to the 109-1671 amino acid polypeptide; or a sequence comprising one or more conservative substitutions in the 109-1671 amino acid polypeptide. The invention further comprises: a composition; a kit comprising the composition; a method for determining the presence or amount of the polypeptide or nucleic acid molecule in a sample; determining the presence of, or predisposition to, a disease associated with the altered levels of nucleic acid or of expression of the polypeptide in a first mammalian subject; identification of an agent that binds to the polypeptide; identification of a potential therapeutic agent for treating a pathology related to aberrant expression or physiological interactions of the polypeptide; a method of screening for a modulator of activity or latency of, or predisposition to, a pathology associated with the polypeptide; a method for modulating the activity of the polypeptide; treating or preventing a pathological state in a mammal; an isolated nucleic acid molecule; a vector comprising the nucleic acid molecule; a cell comprising the vector; an antibody that immunospecifically binds to the polypeptide; and a method for producing the polypeptide. The NOVX polypeptide and its encoding nucleic acid have cytostatic activity. The NOVX polynucleotide can be used in gene therapy to treat disorders. The NOVX polypeptide can be used to create a vaccine. The polypeptide is useful for preparing a composition for treating or preventing a pathological state in a mammal, e.g., cancer, or for chromosome mapping. This sequence represents a NOVX polypeptide of the invention.
CC	Sequence 273 AA;	XX	Sequence 278 AA;
CC	Query Match 54.4%; Score 181; DB 7; Length 273;	XX	Query Match 54.4%; Score 181; DB 7; Length 278;
CC	Best Local Similarity 97.2%; Pred. No. 3_66-12;	XX	Best Local Similarity 97.2%; Pred. No. 3_7e-12;
CC	Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;	XX	Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy	5 ATEVFTPVPTVDTYDGRGDSVYGRSSKSKKFRRP 40	XX	5 ATEVFTPVPTVDTYDGRGDSVYGRSSKSKKFRRP 40
Db	101 ATEVFTPVPTVDTYDGRGDSVYGRSSKSKKFRRP 136	XX	128 ATEVFTPVPTVDTYDGRGDSVYGRSSKSKKFRRP 163
SQ	03-OCT-2003.	XX	03-OCT-2003.
RESULT 13	03-JUN-2004 (first entry)	XX	03-JUN-2004 (first entry)
ADM47287	DT Obteoponcin like NOVX 11b protein.	XX	DT Obteoponcin like NOVX 11b protein.
ID	ADM47287 standard; protein; 278 AA.	XX	DE
XX	Unidentified.	XX	DE
XX	W02003083039-A2.	OS	DE
XX	09-OCT-2003.	OS	DE
XX	03-JUL-2002; 2002WO-US021485.	OS	DE
XX	05-JUL-2001; 2001US-0303046P.	OS	DE
PR	09-JUL-2001; 2001US-0303828P.	OS	DE
PR	11-JUL-2001; 2001US-0304502P.	OS	DE
PR	12-JUL-2001; 2001US-0305011P.	OS	DE
PR	13-JUL-2001; 2001US-0305262P.	OS	DE
PR	16-JUL-2001; 2001US-0305673P.	OS	DE
PR	24-JUL-2001; 2001US-0306085P.	OS	DE
PR	27-JUL-2001; 2001US-0307536P.	OS	DE
PR	30-JUL-2001; 2001US-0308228P.	OS	DE
PR	14-AUG-2001; 2001US-0312203P.	OS	DE
PR	17-SEP-2001; 2001US-032640P.	OS	DE
PR	19-SEP-2001; 2001US-0323484P.	OS	DE
PR	21-SEP-2001; 2001US-0323821P.	OS	DE
PR	21-SEP-2001; 2001US-0323948P.	OS	DE
PR	09-OCT-2001; 2001US-0327891P.	OS	DE
Qy	Sequence 278 AA;	XX	Sequence 278 AA;
Db	Query Match 54.4%; Score 181; DB 7; Length 278;	XX	Query Match 54.4%; Score 181; DB 7; Length 278;
Db	Best Local Similarity 97.2%; Pred. No. 3_7e-12;	XX	Best Local Similarity 97.2%; Pred. No. 3_7e-12;
Db	Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;	XX	Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

RESULT 14
 ADS10984 standard; protein: 279 AA.
 XX
 ADS10984;
 AC
 XX
 DT 16-DEC-2004 (first entry)
 XX
 DE Human therapeutic protein - SEQ ID 1221.
 XX
 KW antiinflammatory; neuroprotective; antianaeamic; cytosstatic; vulnerable;
 KW inflammatory; haemopoiesis; immunity; neurodegenerative; stem cell;
 KW aplastic anaemia; cancer; wound healing; gene therapy.
 XX
 OS Homo sapiens.
 XX
 PN WO2004080148-A2.
 XX
 PD 23-SEP-2004.
 XX
 PR 30-SEP-2003; 2003WO-US030720.
 XX
 PR 02-OCT-2002; 2002US-0416186P.
 XX
 PA (NUVEO) NUVEO INC.
 XX
 PI Tang YT, Asundi V, Ren F, Zhang J, Wehrman T, Wang Z, Ma Y, Wang D, Chen R, Zhao QA, Wang J, Ghosh M, Xue AJ, Weng G, Zhou P, WPI; 2004668857/65.
 DR N-PSDB; ADS10300.
 XX
 PR New polynucleotide, useful in preparing a composition for diagnosing or
 PR treating inflammatory, neurodegenerative or stem cell disorders, e.g.,
 PR aplastic anaemia or cancer for promoting wound healing.
 XX
 PS Claim 20; SEQ ID NO 1221; 718pp; English.
 XX
 CC The invention relates to a novel isolated polynucleotide and the encoded
 CC polypeptide. The molecules of the invention demonstrate antiinflammatory,
 CC neuroprotective, antianaeamic, cytosstatic and vulnerable activities and may
 CC be useful in preparing a composition for diagnosing or treating
 CC inflammatory, hematopoietic, immune, neurodegenerative or stem cell
 CC disorders, such as aplastic anaemia or cancer, as well as for promoting
 CC wound healing. The molecules may also be utilized during gene therapy
 CC procedures. The current sequence is that of a human therapeutic protein
 CC of the invention. The current sequence is not shown explicitly within the
 CC specification but can be accessed from the WIPO web-site.
 XX
 Sequence 279 AA;

OS Homo sapiens.
 XX
 PN WO9222316-A1.
 XX
 AC
 XX
 DT 23-DEC-1992.
 XX
 PR 01-JUN-1992; 92WO-US04599.
 XX
 PR 10-JUN-1991; 91US-00712476.
 XX
 PA (CHIL-) CHILDRENS HOSPITAL PHILADELPHIA.
 PA (UYPE-) UNIV PENNSYLVANIA.
 PA (UYCA-) UNIV CAMBRIDGE.
 XX
 PI Hoye J, Neilson E, Sinclair J, Clayman M, Shiraga H,
 PI Borysiewicz L;
 XX
 DR WPI; 1993-017903/02.
 XX
 PT Compsn, for treating kidney stone diseases, osteoporosis, etc. - contains
 PT aspartic acid-rich protein, and proteins having homology of active
 PT portions.
 XX
 Disclosure; Page 41; 65pp; English.
 XX
 CC To protein is an isoform of human osteopontin (see Young, et al., 'Genomics, Vol. 7, pp. 491-502, 1990). The last 4 amino acids of the HUP
 CC sequences are deleted from the isoform encoded by mRNA from human bone,
 CC decidua and kidney. The sequence may be used to design probes and primers
 CC for the isolation of HUP DNA. See also AAR30700. (Updated on 25-MAR-2003
 CC to correct PN field.)
 XX
 Sequence 282 AA;

Query Match 54.4%; Score 181; DB 2; Length 282;
 Best Local Similarity 97.2%; Pred. No. 3.7e-12;
 Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 5 ATEVFTPVVPTVDTYDGRGDSVYGRRSKSKKFRRP 40
 Db 110 ATEVFTPVVPTVDTYDGRGDSVYGRRSKSKKFRRP 145

Search completed: July 27, 2005, 18:11:55
 Job time: 168 sec

RESULT 15
 AAR30701 standard; protein: 282 AA.
 XX
 AAR30701;
 XX
 DT 25-MAR-2003 (revised)
 DT 14-MAY-1993 (first entry)
 XX
 DE Isoform of human osteopontin protein.
 XX
 KW Human; HUP; osteopontin; kidney stone; osteoporosis.

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OM protein - protein search, using sw model

Run on: July 27, 2005, 18:06:23 ; Search time 42 seconds
(without alignment(s)
111.974 Million cell updates/sec

Title: US-09-981-845-11
Perfect score: 333
Sequence: 1 RSRRATEVFTPVPVPTVTDYD.....AGGPAGPAGPAGPAGPAGPAGPAGPA 63

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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6: /cgn2_6/ptodata/1/iaa/bcteles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB ID	Description
1	181	54.4	282	1	US-07-712-476A-5	Sequence 5, Appli
2	181	54.4	296	1	US-07-712-476A-1	Sequence 1, Appli
3	181	54.4	300	4	US-09-949-016-5962	Sequence 5962, Appli
4	181	54.4	314	4	US-09-134-253-1	Sequence 1, Appli
5	181	54.4	314	4	US-09-205-576-2	Sequence 2, Appli
6	181	54.4	314	4	US-09-538-092-896	Sequence 896, Appli
7	181	54.4	329	4	US-09-949-016-10363	Sequence 10363, Appli
8	177	53.2	300	6	5340934-6	Patent No. 5340934
9	177	53.2	300	6	5340934-6	Patent No. 5340934
10	160	48.0	32	4	US-09-134-253-6	Sequence 6, Appli
11	118	35.4	278	6	5340934-8	Patent No. 5340934
12	118	35.4	278	6	5340934-8	Patent No. 5340934
13	111	33.3	317	4	US-09-485-077A-17	Sequence 17, Appli
14	95.5	28.7	1057	3	US-08-933-820-1	Sequence 1, Appli
15	95.5	28.7	1341	3	US-08-965-825-18	Sequence 18, Appli
16	95.5	28.7	1341	3	US-09-505-811-18	Sequence 18, Appli
17	95.5	28.7	1341	3	US-09-570-573-18	Sequence 18, Appli
18	95.5	28.7	1341	3	US-09-548-608-18	Sequence 18, Appli
19	95.5	28.7	1464	4	US-09-333-347C-21	Sequence 2, Appli
20	91.5	27.5	1024	3	US-08-933-820-2	Sequence 2, Appli
21	91.5	27.5	1366	3	US-08-965-825-19	Sequence 19, Appli
22	91.5	27.5	1366	3	US-09-505-811-19	Sequence 19, Appli
23	91.5	27.5	1366	3	US-09-548-608-19	Sequence 19, Appli
24	91.5	27.5	1366	3	US-09-548-608-19	Sequence 19, Appli
25	91.5	27.5	1366	4	US-09-585-887-10	Sequence 10, Appli
26	91.5	27.5	1366	4	US-09-289-578-10	Sequence 10, Appli
27	91.5	27.5	1366	4	US-09-949-016-5882	Sequence 5882, Appli

ALIGMENTS

RESULT 1
US-07-712-476A-5
; Sequence 5, Application US/07712476A
; Patent No. 5304496
; GENERAL INFORMATION:
; APPLICANT: HOYER et al.
; TITLE OF INVENTION: Biological Regulation of
; TITLE OF INVENTION: Mineralization
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz &
; ADDRESS: No. 530449618
; STREET: One Liberty Place 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19101
; CURRENT APPLICATION DATA:
; COMPUTER READABLE FORM: DISKETTE, 3.5 INCH, 1.44 MB STORAGE
; MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 MB STORAGE
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: PC DOS
; SOFTWARE: WORDPERFECT 5.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/712,476A
; FILING DATE: 19910610
; CLASSIFICATION: 514
; PRIORITY APPLICATION NUMBER:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Suzanne E. Miller
; REGISTRATION NUMBER: 32,279
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 282 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: Linear
; US-07-712-476A-5
; Query Match 54.4%; Score 181; DB 1; Length 282;
; Best Local Similarity 97.2%; Pred. No. 6.5e-13;
; Matches 35; Conservative 0; Mismatches 1;
; Indels 0; Gaps 0;
; Qy 5 ATEVFTPVPTVPTVDTYGRGDSVYGRSKSKKFRP 40
; Db 110 ATEVFTPVPTVPTVDTYGRGDSVYGRSKSKKFRP 145

RESULT 2
US-07-712-476A-1
; Sequence 1, Application US/07712476A

GENERAL INFORMATION:
; APPLICANT: Hoyer, et al.
; TITLE OF INVENTION: Biological Regulation of
; Mineralization
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock, Wasiburn Kurtz Mackiewicz &
; ADDRESS: No. 53049496r8
; STREET: One Liberty Place 46th Floor
; CITY: Philadelphia
; STATE: PA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: PC DOS
; SOFTWARE: WORDPERFECT 5.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/712,476A
; FILING DATE: 19910610
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; NAME: Suzanne E. Miller
; REGISTRATION NUMBER: 32 279
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 568 3100
; TELEFAX: (215) 568 3439
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 296 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
US-07-712-476A-1

Query Match 54.4%; Score 181; DB 1; Length 296;
Best Local Similarity 97.2%; Pred. No. 6.9e-11;
Matches 35; Conservative 0; Mismatches 0; Gaps 0;
Indels 0;

Qy 5 ATEVFTPVVPTVDTYDGRGDSVYGRRSKSKKFRRP 40
Db 124 ATEVFTPVVPTVDTYDGRGDSVYGLRSKSKKFRRP 159

RESULT 3
US-09-949-016-5962
; Sequence 5962, Application US/09949016
; Patent No. 6551946

GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig, et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CLO001307
; CURRENT APPLICATION NUMBER: US/09/949, 016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241, 755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237, 768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231, 498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0

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Best Local Similarity 97.2%; Pred. No. 7.3e-13;
Matches 35; Conservative 0; Mismatches 1; Indels 0;
Gaps 0;

Qy 5 ATEVFTPVVPTVDTYDGRGDSVYGRRSKSKKFRRP 40
Db 142 ATEVFTPVVPTVDTYDGRGDSVYGLRSKSKKFRRP 177

RESULT 4
US-09-134-253-1
; Sequence 1, Application US/09134253
; Patent No. 6569026

GENERAL INFORMATION:
; APPLICANT: Ashkar, Sammy
; TITLE OF INVENTION: Osseopontin Coated Surfaces and Methods of Use
; FILE REFERENCE: CME-100CP
; CURRENT APPLICATION NUMBER: US/09/134,253
; CURRENT FILING DATE: 1998-08-14
; EARLIER APPLICATION NUMBER: 08/916,912
; EARLIER FILING DATE: 1997-08-15
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 314
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-134-253-1

Query Match 54.4%; Score 181; DB 4; Length 314;
Best Local Similarity 97.2%; Pred. No. 7.3e-13;
Matches 35; Conservative 0; Mismatches 0; Gaps 0;

Qy 5 ATEVFTPVVPTVDTYDGRGDSVYGRRSKSKKFRRP 40
Db 142 ATEVFTPVVPTVDTYDGRGDSVYGLRSKSKKFRRP 177

RESULT 5
US-09-206-576-2
; Sequence 2, Application US/09206576
; Patent No. 6551940

GENERAL INFORMATION:
; APPLICANT: Giachelli, Cecilia M.
; FILE REFERENCE: P-UW 3244
; CURRENT APPLICATION NUMBER: US/09/206,576
; CURRENT FILING DATE: 1998-12-07
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 314
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-206-576-2

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Matches 35; Conservative 0; Mismatches 1; Indels 0;
Gaps 0;

Qy 5 ATEVFTPVVPTVDTYDGRGDSVYGRRSKSKKFRRP 40
Db 142 ATEVFTPVVPTVDTYDGRGDSVYGLRSKSKKFRRP 177

RESULT 6

Patent No. 5340934
 ; APPLICANT: TERMINE, JOHN D.; YOUNG, MARIAN F.; FISHER, LARRY W.
 ; ROBEY, PAMELA G.
 ; TITLE OF INVENTION: CDNA SEQUENCES OF HUMAN BONE MATRIX PROTEINS
 ; NUMBER OF SEQUENCES: 13
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/07/432,044
 ; FILING DATE: 03-NOV-1989
 ; SEQ ID NO.: 5340934-8
 ; LENGTH: 278

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 Best Local Similarity 68.8%; Pred. No. 9.2e-06; Indels 0; Gaps 0;

Qy 8 VFTPPVVPVDTYDGRGDSVYGRRSKSKFRR 39
 Db 138 VFTPPFIPESANDGRGDSVAYGLKSRSKSKFRR 169

5340934-8

RESULT 12
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 ; Patent No. 5340934
 ; APPLICANT: TERMINE, JOHN D.; YOUNG, MARIAN F.; FISHER, LARRY W.
 ; ROBEY, PAMELA G.
 ; TITLE OF INVENTION: CDNA SEQUENCES OF HUMAN BONE MATRIX PROTEINS
 ; NUMBER OF SEQUENCES: 13
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/07/432,044
 ; FILING DATE: 03-NOV-1989
 ; SEQ ID NO.: 5340934-8
 ; LENGTH: 278

Query Match 35.4%; Score 118; DB 6; Length 278;
 Best Local Similarity 68.8%; Pred. No. 9.2e-06; Indels 0; Gaps 0;

Qy 8 VFTPPVVPVDTYDGRGDSVYGRRSKSKFRR 39
 Db 138 VFTPPFIPESANDGRGDSVAYGLKSRSKSKFRR 169

5340934-8

RESULT 13
 US-09-485-077A-17
 ; Sequence 17, Application US/09485077A
 ; GENERAL INFORMATION:
 ; APPLICANT: Mukherjee, Anil
 ; APPLICANT: Panda, Dibyendu
 ; APPLICANT: Kundu, Gopal
 ; TITLE OF INVENTION: Methods and Compositions for Treatment of Restenosis
 ; CURRENT APPLICATION NUMBER: US/09/485,077A
 ; CURRENT FILING DATE: 2000-06-23
 ; PRIOR APPLICATION NUMBER: PCT/US98/16569
 ; PRIOR FILING DATE: 1998-07-08
 ; PRIOR APPLICATION NUMBER: 60/054,967
 ; NUMBER OF SEQ ID NOS: 18
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO: 17
 ; LENGTH: 317
 ; TYPE: PRT
 ; ORGANISM: Rattus No. 6458590vegicus

US-09-485-077A-17

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Job time : 46 sec

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OM protein - protein search, using sw model

Run on: July 27, 2005, 18:14:59 ; Search time 154 Seconds (without alignments)

159.133 Million cell updates/sec

Title: US-09-981-845-11

Perfect score: 333

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RESULT 1
US-10-220-107-6

; Sequence 6, Application US/10220107

; Publication No. US20040034195A1

; GENERAL INFORMATION:

; APPLICANT: Ashkar, Samy

; APPLICANT: Hikita, Sherry

; APPLICANT: Dehnl, Ghassan

; TITLE OF INVENTION: Biosynthetic Oncolytic Molecules and Uses Therefor

; FILE REFERENCE: CMCC 725

; CURRENT APPLICATION NUMBER: US/10/220,107

; CURRENT FILING DATE: 2002-08-28

; NUMBER OF SEQ ID NOS: 8

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 6

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE: OTHER INFORMATION: Synthetic Peptide

; US-10-220-107-6

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	236	70.9	87	15 US-10-220-107-6	Sequence 6, Appli
2	236	70.9	87	17 US-10-900-512-6	Sequence 6, Appli
3	181	54.4	192	9 US-09-805-020-41	Sequence 41, Appli
4	181	54.4	278	15 US-10-177-975-120	Sequence 120, Appli
5	181	54.4	286	16 US-10-477-876-3	Sequence 3, Appli
6	181	54.4	287	14 US-10-073-340-231	Sequence 231, Appli
7	181	54.4	287	14 US-10-171-311-176	Sequence 176, Appli
8	181	54.4	287	14 US-10-205-822-307	Sequence 307, Appli
9	181	54.4	287	14 US-10-177-293-340	Sequence 340, Appli
10	181	54.4	287	14 US-10-317-822-147	Sequence 147, Appli
11	181	54.4	287	16 US-10-678-355-6	Sequence 6, Appli

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

ALIGNMENTS

Sequence 48, Appli

Sequence 2, Appli

Sequence 2, Appli

Sequence 229, Appli

Sequence 174, Appli

Sequence 305, Appli

Sequence 338, Appli

Sequence 145, Appli

Sequence 267, Appli

Sequence 504, Appli

Sequence 1333, Appli

Sequence 12, Appli

Sequence 15, Appli

Sequence 15, Appli

Sequence 1, Appli

Sequence 4, Appli

Sequence 8, Appli

Sequence 75, Appli

Sequence 31, Appli

Sequence 22, Appli

Sequence 42, Appli

Sequence 90, Appli

Sequence 2, Appli

Sequence 10, Appli

Sequence 24, Appli

Sequence 227, Appli

Sequence 172, Appli

Sequence 1, Appli

Sequence 303, Appli

Sequence 336, Appli

Sequence 60, Appli

Sequence 143, Appli

Sequence 1, Appli

Sequence 1, Appli

Sequence 255-027-1333

Sequence 10-057-080-12

Sequence 1-229-345-15

Sequence 10-301-822-145

Sequence 10-170-385-267

Sequence 10-25-027-508

Sequence 10-057-080-12

Sequence 10-177-177-15

Sequence 10-650-112-15

Sequence 10-712-124-90

Sequence 10-678-355-4

Sequence 10-764-649-8

Sequence 10-734-560-75

Sequence 10-690-880-31

Sequence 10-818-666-22

Sequence 10-849-989-42

Sequence 10-918-000A-24

Sequence 10-097-340-227

Sequence 10-171-311-172

Sequence 10-303-583-1

Sequence 10-205-823-303

Sequence 10-177-293-336

Sequence 10-241-220-60

Sequence 10-301-822-143

Sequence 10-376-383-2

Sequence 10-239-555-1

Sequence 10-220-107-1

i TITLE OF INVENTION: disease8
 i FILE REFERENCE: WO 473
 i CURRENT APPLICATION NUMBER: US/10/477, 876
 i CURRENT FILING DATE: 2003-11-17
 i PRIOR APPLICATION NUMBER: 01111296
 i PRIOR FILING DATE: 2001-05-17
 i NUMBER OF SEQ ID NOS: 5
 i SOFTWARE: PatentIn version 3.1
 i SEQ ID NO: 3
 i LENGTH: 286
 i TYPE: PRT
 i ORGANISM: Homo sapiens
 i US-10-477-876-3

Query Match 54.4%; Score 181; DB 16; Length 286;
 Best Local Similarity 97.2%; Pred. No. 7.8e-11; Indels 0; Gaps 0;

Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

RESULT 7
 US-10-171-311-176
 i Sequence 176, Application US/10171311
 i Publication No. US20030087270A1
 i GENERAL INFORMATION:
 i APPLICANT: Schlegel, Robert
 i APPLICANT: Chen, Yan
 i APPLICANT: Zhao, Xumei
 i APPLICANT: Monahan, John
 i APPLICANT: Kamatkar, Shubhangi
 i APPLICANT: Glatt, Karen
 i APPLICANT: Gannavarapu, Manjula
 i APPLICANT: Hoersch, Sebastian
 i TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR THERAPY OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF CERVICAL CANCER

i FILE REFERENCE: MRI-035
 i CURRENT APPLICATION NUMBER: US/10/171, 311
 i CURRENT FILING DATE: 2002-06-12
 i PRIORITY NUMBER: US 60/298, 159
 i PRIORITY FILING DATE: 2001-06-13
 i PRIORITY APPLICATION NUMBER: US 60/298, 155
 i PRIORITY FILING DATE: 2001-06-13
 i PRIORITY APPLICATION NUMBER: US 60/335, 936
 i PRIORITY FILING DATE: 2001-11-14
 i NUMBER OF SEQ ID NOS: 218
 i SOFTWARE: Fast-SEQ for Windows Version 4.0
 i SEQ ID NO: 176
 i LENGTH: 287
 i TYPE: PRT
 i ORGANISM: Homo sapiens
 i US-10-171-311-176

Query Match 54.4%; Score 181; DB 14; Length 287;
 Best Local Similarity 97.2%; Pred. No. 7.8e-11; Indels 0; Gaps 0;

Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

RESULT 8
 US-10-205-823-307
 i Sequence 307, Application US/10205823
 i Publication No. US20030108963A1
 i GENERAL INFORMATION:
 i APPLICANT: Schlegel, Robert
 i APPLICANT: Monahan, John E.
 i APPLICANT: Eidege, Wilson O.
 i APPLICANT: Gannavarapu, Manjula
 i APPLICANT: Gorbacheva, Bella
 i APPLICANT: Hoersch, Sebastian
 i APPLICANT: Kamatkar, Shubhangi
 i APPLICANT: Wonsley, Angela M.
 i APPLICANT: Glatt, Karen
 i APPLICANT: Zhao, Xumei
 i APPLICANT: Anderson, Dustin
 i TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF PROSTATE CANCER

i FILE REFERENCE: MRI-044
 i CURRENT APPLICATION NUMBER: US/10/205, 823
 i CURRENT FILING DATE: 2002-07-25
 i PRIORITY NUMBER: 60/307, 982
 i PRIORITY FILING DATE: 2001-07-25

Query Match 54.4%; Score 181; DB 14; Length 287;
 Best Local Similarity 97.2%; Pred. No. 7.8e-11;
 i SEQ ID NO: 363
 i SOFTWARE: Fast-SEQ for Windows Version 4.0
 i LENGTH: 287
 i TYPE: PRT
 i ORGANISM: Homo sapiens
 i US-10-097-340-231

```

; PRIOR APPLICATION NUMBER: 60/314,356
; PRIOR FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: 60/325,020
; PRIOR FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: 60/341,746
; PRIOR FILING DATE: 2001-12-12
; PRIOR APPLICATION NUMBER: 60/362,158
; PRIOR FILING DATE: 2002-03-05
; NUMBER OF SEQ ID NOS: 455
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO: 307
; LENGTH: 287
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-205-823-307
Query Match 54.4%; Score 181; DB 14; Length 287;
Best Local Similarity 97.2%; Pred. No. 7.8e-11;
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
; Gaps 0;
; Gaps 0;

RESULT 10
US-10-301-822-147
; Sequence 147, Application US/10301822
; Publication No. US20030148410A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: Berger, Allison
; APPLICANT: Guillemette, Tracy L.
; APPLICANT: Kamatkar, Shubhangi
; APPLICANT: Schlesel, Robert
; APPLICANT: Monahan, John E.
; APPLICANT: Tibodeau, Lawrence J.
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS AND METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND TREATMENT OF COLON CANCER
; FILE REFERENCE: NPM01-029P2RNW
; CURRENT APPLICATION NUMBER: US/10/301,822
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 60/339,971
; PRIOR FILING DATE: 2001-12-10
; PRIOR APPLICATION NUMBER: US 60/361,978
; PRIOR FILING DATE: 2002-03-05
; PRIOR APPLICATION NUMBER: US 60/381,988
; PRIOR FILING DATE: 2002-05-20
; NUMBER OF SEQ ID NOS: 228
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO: 147
; LENGTH: 287
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-301-822-147

Query Match 54.4%; Score 181; DB 14; Length 287;
Best Local Similarity 97.2%; Pred. No. 7.8e-11;
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
; Gaps 0;
; Gaps 0;

RESULT 9
US-10-177-293-340
; Sequence 340, Application US/10177293
; Publication No. US20030124128A1
; GENERAL INFORMATION:
; APPLICANT: Lillie, James
; APPLICANT: Glatt, Karen
; APPLICANT: Zhao, Xumei
; APPLICANT: Gannavarpu, Manjula
; APPLICANT: Kamatkar, Shubhangi
; APPLICANT: Mertens, Maureen
; APPLICANT: Myer, Vic
; APPLICANT: Wang, Youzhen
; APPLICANT: Hoersch, Sebastian
; APPLICANT: Monahan, John
; APPLICANT: Meyers, Rachel E.
; APPLICANT: Bast Jr., Robert C.
; APPLICANT: Hortobagyi, Gabriel N.
; APPLICANT: Pusztai, Lajos
; APPLICANT: Meric, Funda
; APPLICANT: Sahn, Aysegul
; APPLICANT: Mills, Gordon B.
; TITLE OF INVENTION: COMPOSITIONS, KITS, AND METHODS FOR IDENTIFICATION, ASSESSMENT, TREATMENT OF BREAST CANCER
; FILE REFERENCE: MRL-038
; CURRENT APPLICATION NUMBER: US/10/177,293
; CURRENT FILING DATE: 2002-06-21
; PRIOR APPLICATION NUMBER: US 60/299,887
; PRIOR FILING DATE: 2001-06-21
; PRIOR APPLICATION NUMBER: US 60/301,572
; PRIOR FILING DATE: 2001-06-27
; PRIOR APPLICATION NUMBER: US 60/306,501
; PRIOR FILING DATE: 2001-07-18
; PRIOR APPLICATION NUMBER: US 60/325,002
; PRIOR FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: US 60/362,585
; PRIOR FILING DATE: 2002-03-05
; PRIOR APPLICATION NUMBER: US 60/xxxx,xxx
; NUMBER OF SEQ ID NOS: 506
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO: 340
; LENGTH: 287
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-177-293-340
Query Match 54.4%; Score 181; DB 16; Length 287;
Best Local Similarity 97.2%; Pred. No. 7.8e-11;

```


RESULT 15
 US-10-097-340-229
 Sequence 229, Application US/10097340
 Publication No. US20030087250A1
 GENERAL INFORMATION:
 APPLICANT: John MONAHAN
 APPLICANT: Manjula GANNAVAPU
 APPLICANT: Sebastian HOERSCH
 APPLICANT: Shubhangi KAMATKAR
 APPLICANT: Steve G. KOVATS
 APPLICANT: Rachel E. MEYERS
 APPLICANT: Michael MORRISEY
 APPLICANT: Peter OLANDT
 APPLICANT: Ami SEN
 APPLICANT: Peter VEIBY
 APPLICANT: Gordon B. MILLS
 APPLICANT: Robert C. BAST, JR.
 APPLICANT: Karen LU
 APPLICANT: Rosemarie SCHMANDT
 APPLICANT: Xumei ZHAO
 APPLICANT: Karen GLAFT
 TITLE OF INVENTION: Nucleic Acid Molecules and Proteins For The Identification, Assessment, Prevention, and Therapy of Ovarian Cancer
 FILE REFERENCE: MRI-030
 CURRENT APPLICATION NUMBER: US/10/097,340
 CURRENT FILING DATE: 2002-03-14
 PRIOR APPLICATION NUMBER: 60/276,025
 PRIOR FILING DATE: 2001-03-14
 PRIOR APPLICATION NUMBER: 60/325,149
 PRIOR FILING DATE: 2001-09-26
 PRIOR APPLICATION NUMBER: 60/276,026
 PRIOR FILING DATE: 2001-03-14
 PRIOR APPLICATION NUMBER: 60/324,967
 PRIOR FILING DATE: 2001/09/26
 PRIOR APPLICATION NUMBER: 60/311,732
 PRIOR FILING DATE: 2001-08-10
 PRIOR APPLICATION NUMBER: 60/325,102
 PRIOR FILING DATE: 2001-09-16
 PRIOR APPLICATION NUMBER: 60/323,580
 PRIOR FILING DATE: 2001-09-19
 NUMBER OF SEQ ID NOS: 363
 SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO 229
 LENGTH: 300
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-10-097-340-229

Query Match 54.4%; Score 181; DB 14; Length 300;
 Best Local Similarity 97.2%; Pred. No. 8.2e-11;
 Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Qy 5 ATEVFTPVPTVPTDGRGDSVYGRKSKSKEFRRP 40
 Db 128 ATEVFTPVPTVPTDGRGDSVYGRKSKSKEFRRP 163

Search completed: July 27, 2005, 18:28:26
 Job time : 155 sec

GenCore version 5.1.6
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run on: July 27, 2005, 18:05:17 ; Search time 39 Seconds
 (without alignments)
 155.427 Million cell updates/sec

title: US-09-981-845-11

perfect score: 333

sequence: 1 RSRRATEVFTPVPTVTDYD.....ACGGPAGPAGPAGPAGPA 63

scoring table: BLOSUM62

GapOp 10.0 , Gapext 0.5

searched: 283416 seqs, 96216763 residues

total number of hits satisfying chosen parameters: 283416

DB seq length: 0
 minimum DB seq length: 2000000000

post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

database : PTR_79_*

1: PirI:
 2: PirI:
 3: Pir3:
 4: PirI:
 5: PirI:
 6: PirI:
 7: PirI:
 8: PirI:
 9: PirI:
 10: PirI:
 11: PirI:
 12: PirI:
 13: PirI:
 14: PirI:
 15: PirI:
 16: PirI:
 17: PirI:
 18: PirI:
 19: PirI:
 20: PirI:
 21: PirI:
 22: PirI:
 23: PirI:
 24: PirI:
 25: PirI:
 26: PirI:
 27: PirI:
 28: PirI:
 29: PirI:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

result No.	Score	Query	Match	Length	DB	ID	Description
1	181	54.4	314	1	S09575		osteopontin precursor
2	128.5	38.6	303	1	GBPGO		osteopontin precursor
3	121.5	36.5	311	1	JC1191		osteopontin precursor
4	118	35.4	278	1	J50638		osteopontin precursor
5	114	34.2	407	2	G90907		probable tail fiber
6	113	33.9	294	1	A37818		osteopontin precursor
7	111	33.3	301	2	JC5811		osteopontin - rat
8	111	33.3	317	1	A25917		osteopontin precursor
9	107.5	32.3	366	2	S11449		collagen short chain
10	107.5	32.3	423	2	A41207		collagen 13, noncollagen alpha 1 (
11	98	29.4	1039	2	T35878		hypothetical protein
12	97	29.1	437	2	H90854		probable tail fiber
13	97	29.1	439	2	C97069		probable tail fiber
14	96	28.8	1464	2	S59856		collagen alpha 1 (
15	95.5	28.7	1464	1	CGH115		collagen alpha 1 (
16	95.5	28.7	1486	1	B40333		hypothetical protein
17	95	28.5	283	2	T32921		hypothetical protein
18	95	28.5	294	2	T29838		hypothetical protein
19	94	28.2	361	2	H90877		hypothetical protein
20	94	28.2	437	2	E90996		hypothetical protein
21	94	28.2	439	2	A85719		SLH family protein
22	94	28.2	439	2	A85741		probable tail fiber
23	93	27.9	283	2	T29837		probable tail fiber
24	93	27.9	294	2	T29839		probable tail fiber
25	93	27.9	375	2	G86531		probable tail fiber
26	93	27.9	423	2	C75434		probable tail fiber
27	93	27.9	437	2	E90968		probable tail fiber
28	93	27.9	438	2	S53787		probable tail fiber
29	93	27.9	439	2	E85816		probable tail fiber

0	0	316	2	T20497
92.5	27.8	228	2	A44982
1	92	473	2	I50629
2	92	1042	1	CGCH1S
3	92	1453	2	S21626
4	92	291	2	T20942
5	91.5	27.5	2	150694
6	91.5	886	1	CGB076
7	91.5	1049	1	
8	91	1366	1	CCHU2S
9	91	145	2	T08435
0	91	27.3	301	B31219
1	90.5	27.2	103	C34770
2	90.5	27.2	460	T33110
3	90.5	27.2	779	1
4	90	27.0	286	CGB01S
5	90	27.0	297	S34665
				T27525

ALIGNMENTS

PIR 79:*						
database :	Listing First 45 summaries					
result No.	Score	Query Match	Length	DB	ID	Description
1	181	54.4	314	1	S09575	osteopontin precursor
2	128.5	38.6	303	1	GBPGO	osteopontin precursor
3	121.5	36.5	311	1	J51191	osteopontin precursor
4	118	35.4	278	1	JS0638	probable tail fiber
5	114	34.2	407	2	G90907	osteopontin precursor
6	113	33.9	294	1	A37818	osteopontin precursor
7	111	33.3	301	2	JC5811	osteopontin - rat
8	111	33.3	317	1	A25917	osteopontin precursor
9	107.5	32.3	366	2	S11449	collagen short chain
10	107.5	32.3	423	2	A41207	collagen 13, nonf
11	98	29.4	1039	2	T3878	hypothetical protein
12	97	29.1	437	2	H90854	probable tail fiber
13	97	29.1	439	2	H90769	probable tail fiber
14	96	28.8	1464	2	S59856	collagen alpha 1(I)
15	95.5	28.7	1464	1	CGHUI5	collagen alpha 1(I)
16	95.5	28.7	1486	1	B40333	collagen alpha 1(I)
17	95	28.5	283	2	T329221	hypothetical protein
18	95	28.5	294	2	T29838	hypothetical protein
19	94	28.2	361	2	H90877	probable tail fiber
20	94	28.2	437	2	B90996	probable tail fiber
21	94	28.2	439	2	A85719	probable tail fiber
22	94	28.2	439	2	A85741	hypothetical protein
23	93	27.9	283	2	T29837	hypothetical protein
24	93	27.9	294	2	T29839	hypothetical protein
25	93	27.9	375	2	G85341	hypothetical protein
26	93	27.9	423	2	C75434	SLH family protein
27	93	27.9	437	2	E90968	probable tail fiber
28	93	27.9	438	2	S53787	collagen alpha chain
29	93	27.9	439	2	ES5816	probable tail fiber

A;Molecule type: protein
 A;Residues: 263-268 <MOR>
 A;Experimental source: skin
 A;Note: attachment of 2-O-alpha-D-glucosyl-O-beta-D-galactose to 5-hydroxylsine
 R;Labhard, M.B.; Hollister, D.W.
 Matrix 10, 124-130, 1990
 A;Title: Segmental amplification of the entire helical and telopeptide regions of the collagen type I pro-alpha 1(I) chain
 A;Reference number: S15989; MUID:90326017; PMID:2374517
 A;Accession: I52905
 A;Status: translated from GB/EMBL/DBBJ
 A;Molecule type: mRNA
 A;Residues: 342-352,'C' 354-359 <WI2>
 A;Cross-references: GB: S64717; NID: g408196
 A;Note: mutant sequence from patient with osteogenesis imperfecta
 R;Bernard, M.P.; Chu, M.L.; Myers, J.C.; Ramirez, P.; Prockop, D.J.
 Biochemistry 22, 5213-5223, 1983
 A;Title: Nucleotide sequences of complementary deoxyribonucleic acids for the proalpha 1(I) collagen
 A;Reference number: A90476; MUID:84080385; PMID:6689127
 A;Accession: A90476
 A;Molecule type: tRNA
 A;Residues: 425-1250,'X',1252-1328,'S',1330-1390,'X',1392-1464 <BER>
 A;Cross-references: GB:K03179; NID:g180391; PMID:AAA1995-1; PID:9180392
 A;Note: sequence partially completed for missing nucleotides by A29439
 R;Chu, M.L.; Gargiulo, V.; Williams, C.J.; Ramirez, P.
 J. Biol. Chem. 260, 69-694, 1985
 A;Title: Multilexon deletion in an osteogenesis imperfecta variant with increased type I
 A;Reference number: A22161; MUID:85104934; PMID:2981843
 A;Accession: A22161
 A;Molecule type: DNA
 A;Residues: 472-594,'R',596-607 <CH3>
 A;Cross-references: GB:K03179; NID:g179612; NID:g179613; PMID:AAA1847-1; PID:91009094
 A;Note: the authors translated the codon CCT for residue 595 as Pro
 R;Wallis, G.A.; Starman, B.J.; Zinn, A.B.; Byers, P.H.
 Am. J. Hum. Genet. 46, 1034-1040, 1990
 A;Title: Variable expression of osteogenesis imperfecta in a nuclear family is explained by a deletion of the proalpha 1(I) chain
 A;Reference number: A35336; MUID:154365; PMID:95187161; PMID:7881420
 A;Accession: A35336
 A;Molecule type: DNA
 A;Residues: 710-720,'B',722-737,'B',739-745 <WAL>
 A;Note: the authors translated the codons CAG for 721 and CGT for 738 as Glu
 R;Forlino, A.; Zolezzi, F.; Valti, M.; Pignatti, P.F.; Cetta, G.; Brunelli, P.C.; Mottes, H.; Mol. Genet. 3, 2201-2206, 1994
 A;Title: Severe (type III) osteogenesis imperfecta due to glycine substitutions in the collagen type I proalpha 1(I) chain
 A;Reference number: I54365; MUID:9332792; PMID:2339700
 A;Accession: I54365
 A;Status: translated from GB/EMBL/DBBJ
 A;Molecule type: DNA
 A;Residues: 746-766,'S',768-781 <FOR>
 A;Cross-references: GB:K47667; NID:g1009093; PMID:AB59576-1; PMID:91009094
 R;Chessler, S.D.; Wallis, G.A.; Byers, P.H.
 J. Biol. Chem. 268, 1818-1825, 1993
 A;Title: Mutations in the carboxyl-terminal propeptide of the pro alpha 1(I) chain of type I
 A;Reference number: A47426; MUID:9332646; PMID:8343697
 A;Accession: A47426
 A;Molecule type: mRNA
 A;Residues: 1179-1276,'H',1278-1336,1339-1387,'R',1289-1464 <CH4>
 A;Cross-references: GB:IS6456; NID:g107856-1; PMID:9407590
 A;Note: sequence extracted from NCBI backbone (NCBIn:13644, NCBIP:13644)
 A;Note: does not represent an experimentally determined sequence but three different mutant
 A;Accession: B47426
 A;Molecule type: mRNA
 A;Residues: 1179-1464 <CH4>
 A;Experimental source: normal dermal fibroblast culture
 A;Accession: C47426
 A;Molecule type: mRNA

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OM protein - protein search, using sw model

Run on: July 27, 2005, 17:57:07 ; Search time 169 Seconds (without alignments)

190.893 Million cell updates/sec

Title: US-09-981-845-11

Perfect score: 333

Sequence: 1 RSRATEVFTPVVPTVTDYD.....AGGPGAGPAGPAGPAGPA 63

Scoring table: BIOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt_03:
1: uniprot_sprot:
2: uniprot_trembl:
* Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB	ID	Description
1	181	54.4	314	1	OSTP HUMAN	P10451	homo sapien
2	128.5	38.6	105	2	Q9T83	Q9T83	Q9T83
3	128.5	38.6	303	1	OSTP PIG	P14287	sus scrofa
4	121.5	36.5	311	1	OSTP RABBIT	P21097	oryctolagus cuniculus
5	121	36.3	278	1	OSTP SHEEP	Q5asy9	ovis aries
6	118	35.4	278	1	OSTP BOVINE	Q9lh4	bos taurus
7	118	35.4	279	1	OSTP BOS TAU	P31096	bos taurus
8	118	35.4	279	1	Q64125	Q64125	mus musculus
9	118	35.4	295	2	Q6PK83	Q6PK83	mus musculus
10	114	34.2	407	2	Q8XKF6	Q8XKF6	escherichia coli
11	113	33.9	294	1	OSTP MOUSE	P10923	mus musculus
12	111	33.3	165	2	Q6N617	Q6N617	rhodopspseudo
13	111	33.3	317	1	OSTP RAT	P08721	rattus norvegicus
14	111	33.3	317	2	P97827	P97827	rattus norvegicus
15	108	32.4	200	2	Q6XU29	Q6XU29	feldmannia
16	108	32.4	358	2	Q9J3U4	Q9J3U4	ectocarpus
17	107.5	32.3	366	1	CAS4_EPHMU	P18503	ephydatia
18	107.5	32.3	422	2	Q24593	Q24593	m
19	104	31.2	180	2	Q7ONL4	Q7ONL4	anopheles gambiae
20	104	31.2	191	2	Q7PN98	Q7PN98	anopheles gambiae
21	99.5	29.9	1445	2	Q93581	Q93581	o93251
22	99	29.7	1321	2	Q72202	Q72202	bacillus cereus
23	98	29.4	305	2	Q9ACN2	Q9ACN2	streptococcus
24	98	29.4	1039	2	Q5O516	Q5O516	streptomyces
25	97.5	29.3	1355	1	CA21_RANCA	CA21_RANCA	ca21
26	97	29.1	437	2	Q8XSD0	Q8XSD0	escherichia
27	97	29.1	439	2	Q7APX3	Q7APX3	Q7afx3
28	97	29.1	604	2	Q91252	Q91252	streptomyces
29	96	28.8	479	2	Q91A62	Q91A62	prophage p
30	96	28.8	998	2	Q8CPM4	Q8CPM4	mus musculus
31	96	28.8	1222	2	Q8KL73	Q8KL73	mus musculus

ALIGNMENTS

RESULT 1		OSTP HUMAN		STANDARD		PRT; 314 AA.	
ID	OSTP_HUMAN	PL0451	Q15681; Q15682; Q8NBK2; Q961Z1;	AC	PL0451; Q15681; Q15682; Q8NBK2; Q961Z1;	DT	01-MAR-1989 (Rel. 10, Created)
DT		01-MAR-1989	(Rel. 10, Last sequence update)	DT	01-MAR-1989 (Rel. 10, Last sequence update)	DT	25-OCT-2004 (Rel. 45, Last annotation update)
DE	Osteopontin precursor (Bone sialoprotein 1) (Secreted phosphoprotein DE 1) (SPP-1) (Urinary stone protein) (Nephropontin) (Urropontin).			DE	Osteopontin precursor (Bone sialoprotein 1) (Secreted phosphoprotein DE 1) (SPP-1) (Urinary stone protein) (Nephropontin) (Urropontin).	DE	
GN	Homo sapiens (Human)			GN	Homo sapiens (Human)	GN	
RA	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butchera; Primates; Catarrhini; Hominidae; Homo.			RA	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butchera; Primates; Catarrhini; Hominidae; Homo.	RA	
NCBI TaxID	6606;			NCBI TaxID	6606;	NCBI TaxID	
RN				RN		RN	
RP	SEQUENCE FROM N.A. (ISOFORM A).			RP	SEQUENCE FROM N.A. (ISOFORM A).	RP	
RP	MEDLINE=89263749; PubMed=2726470;			RP	MEDLINE=90353945; PubMed=1974876;	RP	
RA	Young M.F., Kerr J.M., Termino J.D., Wewer U.M., Wang M.G., Fisher O.W., Fisher L.W.,			RA	Young M.F., Kerr J.M., Termino J.D., Wewer U.M., Wang M.G., Fisher O.W., Fisher L.W.,	RA	
RT	"cDNA cloning, mRNA distribution and heterogeneity, chromosomal location, and RFLP analysis of human osteopontin (OPN)." ;			RT	"cDNA cloning, mRNA distribution and heterogeneity, chromosomal location, and RFLP analysis of human osteopontin (OPN)." ;	RT	
RL	Genomics 7:491-502 (1990).			RL	Genomics 7:491-502 (1990).	RL	
RN				RP	SEQUENCE FROM N.A. (ISOFORM A).	RP	
RP	MEDLINE=92108068; PubMed=1729712;			RP	MEDLINE=92108068; PubMed=1729712;	RP	
RA	Shiraga H., Min W., Vandusen W.J., Clayman M.D., Miner D., Terrell C.H., Sherbotie J.R., Foreman J.W., Przybicki C., Neilson E.G., Hoyer J.R.,			RA	Shiraga H., Min W., Vandusen W.J., Clayman M.D., Miner D., Terrell C.H., Sherbotie J.R., Foreman J.W., Przybicki C., Neilson E.G., Hoyer J.R.,	RA	
RT	"Inhibition of calcium oxalate crystal growth in vitro by uropontin: another member of the aspartic acid-rich protein superfamily." ;			RT	"Inhibition of calcium oxalate crystal growth in vitro by uropontin: another member of the aspartic acid-rich protein superfamily." ;	RT	
RT	Proc. Natl. Acad. Sci. U.S.A. 89:426-430 (1992).			RT	Proc. Natl. Acad. Sci. U.S.A. 89:426-430 (1992).	RT	
RN				RP	SEQUENCE FROM N.A. (ISOFORM A).	RP	
RP	MEDLINE=9539452; PubMed=7665163;			RP	MEDLINE=9539452; PubMed=7665163;	RP	
RA	Crosby A.H., Edwards S.J., Murray J.C., Dixon M.J.,			RA	Crosby A.H., Edwards S.J., Murray J.C., Dixon M.J.,	RA	
RT	"Genomic organization of the human osteopontin gene: exclusion of the locus from a causative role in the pathogenesis of dentinogenesis imperfecta type II." ;			RT	"Genomic organization of the human osteopontin gene: exclusion of the locus from a causative role in the pathogenesis of dentinogenesis imperfecta type II." ;	RT	
RT	Genomics 27:155-160 (1995).			RT	Genomics 27:155-160 (1995).	RT	
RN				RP	SEQUENCE FROM N.A. (ISOFORM A).	RP	
RP	SEQUENCE FROM N.A. (ISOFORM A).			RP	SEQUENCE FROM N.A. (ISOFORM A).	RP	
RC	MEDLINE=9501968; PubMed=7945249;			RC	MEDLINE=9501968; PubMed=7945249;	RC	
RC	Hijiya N., Setoguchi M., Matsuura K., Higuchi Y., Aizuki S., Yamamoto S.;			RC	Hijiya N., Setoguchi M., Matsuura K., Higuchi Y., Aizuki S., Yamamoto S.;	RC	
RT	"Cloning and characterization of the human osteopontin gene and its promoter." ;			RT	"Cloning and characterization of the human osteopontin gene and its promoter." ;	RT	
RT	Biochem. J. 303:255-262 (1994).			RT	Biochem. J. 303:255-262 (1994).	RT	

[6] SEQUENCE FROM N.A. (ISOFORMS A, B AND C).
 RP TISSUE-BRAIN; PubMed=95139605; Published=2003/07/21;
 RX RA Kohri K., Suzuki Y., Yosida K., Yamamoto K., Amasaki N., Yamada T.,
 RA Umezawa T., Iouchi M., Sinchara H., Kurita T.;
 RA "Expression of osteopontin in human glioma. Its correlation with the
 malignancy.",
 RT RT Molecular cloning and sequencing of cDNA encoding urinary stone
 protein, which is identical to osteopontin.",
 RT RL Biophys. Res. Commun. 184:859-864 (1992).
 RL -I- FUNCTION: Binds tightly to hydroxyapatite. Appears to form an
 integral part of the mineralized matrix. Probably important to
 RPL RPL cell-matrix interaction.
 RP CC -I- FUNCTION: Acts as a cytokine involved in enhancing production of
 RPL CC interleukin-gamma and interleukin-12 and reducing production of
 RN CC interleukin-10 and is essential in the pathway that leads to type
 RP CC I immunity (By similarity).
 RC CC -I- SUBUNIT: Ligand for integrin alpha-5/beta-3.
 RX CC -I- SUBCELLULAR LOCATION: Secreted.
 RA CC -I- ALTERNATIVE PRODUCTS:
 RA CC Event=Alternative splicing; Named isoforms=4;
 RA CC Name=A; Synonyms=OPN-a, OP1B;
 RA CC IsoID=PI0451-1; Sequence=Displayed;
 RA CC Name=B; Synonyms=OPN-b, OPIA;
 RA CC IsoID=PI0451-2; Sequence=VSP_003778;
 RA CC Name=C; Synonyms=OPN-c;
 RA CC IsoID=PI0451-3; Sequence=VSP_003777;
 RA CC Name=D;
 RA CC IsoID=PI0451-4; Sequence=VSP_011639;
 RA CC PTM: Extensively phosphorylated on serine residues.
 RA CC PTM: N- and O-Glycosylation.
 RA CC DISEASE: This protein plays a principal role in urinary stone
 formation as the stone matrix.
 RA CC -I- SIMILARITY: Belongs to the osteopontin family.
 RA CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 RA CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 RA CC the European Bioinformatics Institute. There are no restrictions on its
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 RA CC entities requires a license agreement (see <http://www.isb-sib.ch/announce/>
 RA CC or send an email to license@isb-sib.ch).
 RA CC -----
 RA DR X13694; CAA31984; 1;
 RA DR J04785; ARA5974; 1;
 RA DR M83248; AAA17675; 1;
 RA DR U20758; AAA86386; 1;
 RA DR D14813; BAA03554; 1;
 RA DR D28759; BAA05949; 1;
 RA DR D28760; BAA05951; 1;
 RA DR D78761; BAA05951; 1;
 RA DR AF052124; AAC28619; 1;
 RA DR AK075463; BAC11635; 1;
 RA DR BC00706; AAH0706; 1;
 RA DR BC017387; AAH17387; 1;
 RA DR BC022844; AAH22844; 1;
 RA DR PIR; S50520; S05575;
 RA DR Glycosidases; P10451; -;
 RA DR Genew; HGNC:11255; SPP1;
 RA DR H-InvDB; HX004361; -;
 RA DR MIM; 16490; -;
 RA DR GO; CO:0005578; C: extracellular matrix; TAS.
 RA DR GO; CO:0005125; F: cytokine activity; ISS.
 RA DR GO; CO:0005125; F: cytokine activity; ISS.
 RA DR GO; CO:0005083; F: growth factor activity; TAS.
 RA DR GO; CO:0005178; F: integrin binding; NAS.
 RA DR GO; CO:0005916; F: anti-apoptosis; ISS.
 RA DR GO; CO:0007267; F: cell-cell signaling; TAS.
 RA DR GO; CO:0007160; F: cell-matrix adhesion; NAS.
 RA DR GO; CO:0030595; F: immune cell chemotaxis; TAS.
 RA DR GO; CO:0050530; F: induction of positive chemotaxis; TAS.
 RA DR GO; CO:0030502; F: negative regulation of bone mineralization; TAS.
 RA DR GO; CO:0005103; F: specificity; TAS.
 RA DR GO; CO:0042102; F: positive regulation of T-cell proliferation; TAS.
 RA DR GO; CO:004637; F: regulation of myeloid blood cell differentiation; TAS.
 RA DR GO; CO:0042088; P:T-helper 1 type immune response; TAS.
 RA DR InterPro; IPR002038; Osteopontin.

[7] SEQUENCE FROM N.A. (ISOFORM D).
 RP TISSUE-Placenta;
 RX PubMed=14702039; DOI=10.1038/ng1285;
 RA Ota T., Suzuki Y., Nishikawa T., Otsuki T., Sugiyama T., Irie R.,
 RA Wakamatsu S., Hayashi K., Sato H., Nagai K., Kimura K., Makita H.,
 RA Sekine M., Obayashi M., Nishi T., Shiba-hara T., Tanaka T., Ishii S.,
 RA Yamamoto J.-I., Saito K., Kawai Y., Isono Y., Nakamura Y.,
 RA Nagahara K., Murakami K., Yasuda T., Iwayanagi T., Wagatsuma M.,
 RA Shiratori A., Sudo H., Hosogiri T., Kaku Y., Kodaira H., Kondo H.,
 RA Sugawara M., Takahashi M., Kanda K., Yokoi T., Furuy T., Kikkawa E.,
 RA Onura Y., Abe K., Kamihara K., Katsuta N., Sato K., Tanikawa M.,
 RA Yamazaki M., Ninomiyama K., Ishibashi T., Yamashita H., Murakawa K.,
 RA Fujimori K., Tanai H., Kimata M., Watnabe M., Hiraoaka S., Chiba Y.,
 RA Ishida S., Ono Y., Takiuchi S., Watanabe S., Yosida M., Rotuta T.,
 RA Kusano J., Kanehori K., Takahashi S., Fujii A., Hara H., Tanase T.-O.,
 RA Nomura Y., Togoya S., Komai F., Hara R., Takeuchi K., Arita M.,
 RA Imose N., Musashino K., Fujii Y., Osaki K., Hirao M., Ohmori Y.,
 RA Yoshikawa Y., Matsunaga H., Ichihara T., Shiohata N., Sano S.,
 RA Moriya S., Momiyama H., Satoh N., Takami S., Terashima Y., Suzuki O.,
 RA Nakagawa K., Nakanuma T., Itoh T., Shigeta K., Senba T.,
 RA Hishigaki H., Watanabe M., Kawakami B.,
 RA Yamazaki M., Watanabe K., Kumagai A., Itakura S., Fukuzumi Y.,
 RA Fujimori Y., Komiyama M., Tashiro K., Tanigami K.,
 RA Ono T., Yamada K., Fujii Y., Osaki K., Hirao M., Ohmori Y.,
 RA Kawabata A., Hidai T., Kobatake N., Inagaki H., Ikeda Y., Okamoto S.,
 RA Okamoto R., Kawahara T., Noguchi S.,
 RA Matsunaga K., Nakajima Y., Mizuno T., Morinaga M., Sasaki M.,
 RA Togashi T., Oyama M., Hata H., Watanabe M., Komatsu T.,
 RA Mizumura-Sugano J., Sato Y., Shirai T., Takemoto Y., Nakagawa K.,
 RA Okumura K., Nagate T., Nomura N., Kikuchi H., Masuho Y., Yamashita R.,
 RA Nakai K., Yada T., Nakamura Y., Ohara O., Isogai T., Sugano S.;
 RA RT COMPILER sequencing and characterization of 21,243 full-length human
 RN RT cDNAs.
 RP RN [19] SEQUENCE FROM N.A. (ISOFORMS A AND B).
 RC TISSUE-Brain, and Kidney;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.P., Bhat N.K.,
 RA Hopkins R.F., Jordan R., Moore T., Max S.I., Wang J., Heihs F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Brownstein M., Soares M.B., Bonaldo M.F., Casavant T.E.,
 RA Blakesley R.W., Usdin T.B., Tohuyiuk S., Carninci P., Prange C.,
 RA Raha S.S., Loqueland N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muñiz D.M., Sodergren B.J., Lu X., Gibbs R.A.,
 RA Pahie J., Helton B., Kettman J., Madan M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shvchenko Y., Bouffard G.C.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smialius D.E.,
 RA Schnarch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RA RT "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences."
 RA Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 RN SEQUENCE OF 67-278 FROM N.A.

DR	Pfam; PF00865; Osteopontin; 1.	RL	Mol. Immunol. 32:447-448(1995).
DR	PRINTS; PRO0216; OSTEOPOINTIN.	DR	EMBL; S78177; AAB34351.2; -.
DR	SMART; SM0017; OSTEOPOINTIN.	DR	MGD; MGI:98389; Sp1.
DR	PS00884; OSTEOPOINTIN; 1.	DR	GO; 0007155; P:cell adhesion; IEA.
KW	Biomaterialization; Cell adhesion; Cytokine; Direct protein sequencing;	DR	GO; GO:0001503; Possibilification; IBA.
KW	Glycoprotein; Phosphorylation; Sialic acid; Signal.	DR	Intertro; IPR02038; Osteopontin.
FT	SIGNAL 1 16	DR	Pfam; PF00865; Osteopontin; 1.
FT	CHAIN 17	DR	PRINTS; PR00216; OSTEOPOINTIN.
FT	SITE 152	DR	SMART; SM0017; OSTEOPOINTIN; 1.
FT	MOD-RES 152 154	DR	PROSITE; PS00884; OSTEOPOINTIN; 1.
FT	MOD-RES 23	FT	NON-TER 1
FT	MOD-RES 24 23	FT	SEQUENCE 279 AA; 30949 MW; B0EF5855D0AC14A2 CRC64;
FT	MOD-RES 24	SQ	Query Match 35.4%; Score 118; DB 2; Length 279;
FT	MOD-RES 26 24	Best Local Similarity 65.4%; Pred. No. 0.0067;	
FT	MOD-RES 26 26	Matches 21; Conservative 5; Mismatches 6; Indels 0; Gaps 0;	
FT	MOD-RES 27 27	SEQUENCE 279 AA; 30949 MW; B0EF5855D0AC14A2 CRC64;	
FT	MOD-RES 60 60	Query 7 EVFTPVPTVPTDGRGDSVYGRSKSKKPR 38	
FT	MOD-RES 62 62	Db 114 DTFTPVPTVPTDGRGDSVYGRSKSKRSRSGQ 145	
FT	MOD-RES 63 63	RESULT 9	
FT	MOD-RES 76 76	Q6PK3	
FT	MOD-RES 78 78	ID Q6PK3	
FT	MOD-RES 81 81	PRELIMINARY	
FT	MOD-RES 95 95	PRT; 295 AA.	
FT	MOD-RES 100 100	AC Q6PK3;	
FT	MOD-RES 103 103	DT 05-JUL-2004 (TREMBLrel. 27, Created)	
FT	MOD-RES 115 115	DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)	
FT	MOD-RES 121 121	DT 25-OCT-2004 (TREMBLrel. 28, Last annotation update)	
FT	MOD-RES 124 124	DB Hypothetical protein.	
FT	MOD-RES 178 178	OS Mus musculus (Mouse).	
FT	MOD-RES 184 184	OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
FT	MOD-RES 188 188	OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.	
FT	MOD-RES 205 205	OC NCBITaxonID=10090; OX NCBI_Taxid=10090;	
FT	MOD-RES 210 210	RN [1]	
FT	MOD-RES 233 233	RC SEQUENCE FROM N.A.	
FT	MOD-RES 240 240	RC STRAIN=Mix FVB/N; TISSUE=Mammary tumor;	
FT	MOD-RES 245 245	RC MEDLINE=22388227; PubMed=12477932; DOI=10.1073/pnas.242603899;	
FT	MOD-RES 256 256	RC STRAUBER R.D., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Shamen C.M., Schuler G.D., Altenschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J.J., Hsieh F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bandal M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Usain T.B., Toshimori S., Carnavici P., Prange C., Raha S.S., Loquelinio N.A., Peters G.J., Abramson R.D., Mulhaly S.J., Bosak S.A., McIwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Helton E., Kettenbach M., Madan A., Rodriguez S., Sanchez A., Whiting M., Madan A., Young A.C., Bouffard G.G., Blakesley R.W., Touchman J.W., Green B.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmitz J., Myers R.M., Butterfield Y.S., Krzywinski M.I., Skalska S., Smailus D.E., Schein J.E., Jones S.J., Marra M.A.; Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences"; RT and mouse cDNA sequences"; RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).	
FT	CARBOHYD 140 140	RL [2]	
FT	CARBOHYD 145 145	RN SEQUENCE FROM N.A.	
FT	CONFLICT 27 27	RC STRAIN=Mix FVB/N; TISSUE=Mammary tumor;	
FT	CONFLICT 42 42	RC Director MCC Project; RC STRAUBER R.D.; Submitted (AUG-2004) to the EMBL/GenBank/DBJ databases.	
FT	CONFLICT 56 56	RA RA	
FT	SEQUENCE 278 AA; 30949 MW; EAB62A39AGDD8EEF CRC64;	RA RA	
FT	Query Match 35.4%; Score 118; DB 1; Length 278; Best Local Similarity 68.8%; Pred. No. 0.0066; Matches 22; Conservative 3; Mismatches 7; Indels 0; Gaps 0; Qy 8 VFTPVPTVPTDGRGDSVYGRSKSKFRR 39	RA RA	
Db	138 VFTPVPTVPTDGRGDSVYGRSKSKFRR 169	Db 10095; RESULT 8	
Db	138 VFTPVPTVPTDGRGDSVYGRSKSKFRR 169	Qy 8 VFTPVPTVPTDGRGDSVYGRSKSKFRR 39	
OS	Mus sp.	Db 10095; PRELIMINARY; PRT; 279 AA.	
OC	Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.	DR EMBL; BC002113; AAH02113.1; -.	
OC	Name-Sp1; Synonyms-Eta-1/Op; NCBI_TaxID=10095;	DR EMBL; BC008702; AAH0720.1; -.	
OC	SEQUENCE FROM N.A.	DR GO; GO:0005615; C:extracellular space; TAS.	
OC	MEDLINE:95272553; PubMed=7953053; DOI=10.1016/0161-5890(95)00053-H; Ono M., Yamamoto T., Nose M.;	DR Intertro; IPR02038; Osteopontin.	
OC	"Allelic difference in the nucleotide sequence of the Eta-1/Op gene transcript.";	DR Pfam; PF00865; Osteopontin; 1.	

DR PRINTS; PR00216; OSTEOPONTIN.
 DR SMART; SN00017; OSTBO; 1.
 DR PROITE; PS00084; OSTEOPOINTIN; 1.
 KW Hypothetical protein.
 SQ SEQUENCE 295 AA; 32652 MW; B069BBP87CF9A68 CRC64;
 Query Match 35.4%; Score 118; DB 2; Length 295;
 Best Local Similarity 65.6%; Pred. No. 0.0007;
 Matches 21; Conservative 5; Mismatches 6; Indels 0; Gaps 0;
 OY 7 EVFPTVPPVPTVTDGRGDSVYGRSKSKKFR 38
 DB 130 DTFPIPIVPTVTDVPGRDGLAYGLRSKRSFQ 161

RESULT 10

Q8XSF6 PRELIMINARY; PRT; 407 AA.
 AC Q8XSF6;
 DT 01-MAR-2002 (TREMBLrel. 20, Created)
 DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)
 DE Putative tail fiber protein.
 GN OrderdlocusNames=CS2331;
 OS Escherichia coli Q157:H7.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteraceae; Escherichia.
 OX NCBI_TAXID=83334;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=RIMD 0509952 / EHEC;
 MEDLINE=21156231; PubMed=1158795;
 RA Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K.,
 RA Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T.,
 RA Iida T., Takami H., Honda T., Sasaki C., Ogawara N., Yasunaga T.,
 RA Kuhara S., Shiba T., Hattori M., Shinagawa H.,
 RT "Complete genome sequence of enterohemorrhagic Escherichia coli
 O157:H7 and genomic comparison with a laboratory strain K-12.;"
 RL DNA Res. 8:11-22 (2001).
 EMBL; BAB35654.1; -.
 PIR; G9097; G90907.
 GO; GO:0005797; C:cytoplasm; IEA.
 GO; GO:0006817; P:phosphate transport; IEA.
 PFM; PF01391; Collagen_1.
 DR PP06820; Phage fiber C; 1.
 SQ SEQUENCE 407 AA; 41291 MW; D2F6CSE6ABEBC3EE CRC54;
 Query Match 34.2%; Score 114; DB 2; Length 407;
 Best Local Similarity 48.6%; Pred. No. 0.0024;
 Matches 34; Conservative 5; Mismatches 23; Indels 8; Gaps 4;
 OY 1 RSRPATEVTPVPTVTDG-RGDSVYGRRS-KSKFRR---PAGAAG--GPAGPAG 52
 DB 234 QSRTAEEAVNR1PTVPGPQSEPGPAGPQGPKGDGERDTGPAGATGRGPAGDAG 293

RESULT 11

OSTP_MOUSE ID_OSTP_MOUSE STANDARD; PRT; 294 AA.
 AC P10923; P19008;
 DT 01-JUL-1989 (Rel. 11, Created)
 DT 01-JUL-1989 (Rel. 11, Last sequence update)
 DR 25-OCT-2004 (Rel. 45, Last annotation update)
 DE Osteopontin Precursor (Bone sialoprotein 1)
 DE 1) (SPP-1) (Minopontin) (Early T lymphocyte activation 1 protein)
 DE 2) (2AR) (Calcium oxalate crystal growth inhibitor protein).
 GN Name=SPP1; Synonyms=Eta-1, Op, Spp-1;
 OS Mus musculus (Mouse);
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

DR Mammalia; Eutheria; Rodentia; Sciurognathia; Muridae; Murinae; Mus.
 OX NCBI_TAXID=10090;
 RP SEQUENCE FROM N.A.
 RC STRAIN=BALB/C; TISSUE=Liver;
 RX MEDLINE=90354433; PubMed=2187863;
 RA Miyazaki Y., Setoguchi M., Yoshida S.Y., Akizuki S., Yamamoto S.;
 RT "The mouse osteopontin gene. Expression in monocytic lineages and
 complete nucleotide sequence."
 RL J. Biol. Chem. 265:14432-14438 (1990).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Macrophage;
 RX MEDLINE=89223742; PubMed=272465;
 RA Miyazaki Y., Setoguchi M., Yoshida S., Higuchi Y., Akizuki S.,
 RA Yamamoto S.;
 RT "Nucleotide sequence of cDNA for mouse osteopontin-like protein."
 RL Nucleic Acids Res. 17:3298-3298 (1989).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=89255479; PubMed=2722855;
 RA Craig A.M., Smith J.H., Denhardt D.T.;
 RT "Osteopontin, a transformation-associated cell adhesion
 phosphoprotein, is induced by 12-O-tetradecanoylphorbol 13-acetate in
 mouse epidermis."
 RL J. Biol. Chem. 264:9682-9689 (1989).
 RN [4]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=89310352; PubMed=2787378;
 RA Patarcia R., Freeman G.J., Singh R.P., Wei F.-Y., Durfee T.,
 Blattner P., Regnier D.C., Kozak C.A., Mock B.A., Morse H.C. III,
 RA Jerebels T.R., Cantor H., Craig A.M., Smith J.H., Denhardt D.T.;
 RT "Structural and functional studies of the early T lymphocyte
 activation 1 (Eta-1) gene. Definition of a novel T cell-dependent
 response associated with genetic resistance to bacterial infection."
 RL J. Exp. Med. 170:145-161 (1989).
 RN [5]
 RP SEQUENCE FROM N.A.
 RC STRAIN=NMR1; TISSUE=Mammary Gland;
 RX MEDLINE=22388257; PubMed=1247793; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold B.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shemesh C.M., Schuler G.D.,
 RA Altenschul S.P., Zeeberg B., Buerow K.H., Schaefer C.P., Bhat N.K.,
 RA Hopkins R.F., Jordon H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Chee T.B.,
 RA Brownstein M.J., Usdin T.B., Yoshiaki S., Carnincz P., Prange C.,
 RA Raha S.S., Loughran N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalobos D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko A., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grinwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
 RA Schnarch A., Schein J.E., Jones J.M., Marra M.A.,
 RT "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences."
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 RN [6]
 RP SEQUENCE OF 17-37.
 RC TISSUE=Kidney;
 RX MEDLINE=93034441; PubMed=1414495;
 RA Worcester B.M., Blumenthal S.S., Beshensky A.M., Lewand D.L.;
 RT "The calcium oxalate crystal growth inhibitor protein produced by
 mouse kidney cortical cells in culture is osteopontin."
 RL J. Bone Miner. Res. 7:1029-1036 (1992).
 RN [7]
 RP FUNCTION.
 RX MEDLINE=20126376; PubMed=10657301; DOI=10.1126/science.287.5454.860;
 RA Ashkar S., Weber G.F., Panoutsakopoulou V., Sanchirico M.E.,
 RA Jansson M., Zawaideh S., Rittling S.R., Denhardt D.T., Glimcher M.J.,

9
age

RT	and is a novel component of human atherosclerotic plaques .";
RL	J. Clin. Invest. 92:1686-1696 (1993).
CC	-1- FUNCTION: Binds tightly to hydroxyapatite. Appears to form an integral part of the mineralized matrix. Probably important to cell-matrix interaction.
CC	-1- FUNCTION: Acts as a cytokine involved in enhancing production of interferon-gamma and interleukin-12 and reducing production of interleukin-10 and is essential in the pathway that leads to type I immunity (By similarity).
CC	-1- SUBUNIT: Ligand for integrin alpha-V/beta-3.
CC	-1- PTM: Extensively phosphorylated on serine residues.
CC	-1- PTM: N- and O-glycosylated.
CC	-1- SIMILARITY: Belongs to the osteopontin family.
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to licenses@isb-sib.ch).
CC	EMBL: M99252; AAA41765.1; -.
CC	EMBL: M14656; AAA41762.1; -.
CC	DR PIR: A25917; A25917.
CC	DR PIR: A25917; A25917.
CC	DR RGD: 3752; SPP1.
CC	DR GO: GO-0005578; C: extracellular matrix; ISS.
CC	DR GO: GO-0005125; F:cytokine activity; ISS.
CC	DR GO: GO-0008083; F:growth factor activity; ISS.
CC	DR GO: GO-0005178; F:integrin binding; ISS.
CC	DR GO: GO-0006516; F:anti-apoptosis; ISS.
CC	DR GO: GO-0007267; P:cell-cell signalling; ISS.
CC	DR GO: GO-0007160; P:cell-matrix adhesion; ISS.
CC	DR GO: GO-0005930; P:immune cell chemotaxis; ISS.
CC	DR GO: GO-0030502; P:negative regulation of bone mineralization; ISS.
CC	DR GO: GO-0042402; P:positive regulation of T-cell cell differentiation; ISS.
CC	DR GO: GO-0045637; P:regulation of myeloid blood differentiation. . .; ISS.
CC	DR GO: GO-104208; P:T-helper 1 type immune response; ISS.
CC	DR InterPro: IPR02038; Osteopontin.
CC	DR Pfam: PF00365; Osteopontin, 1.
CC	DR PRINTS: PR00216; OSTEPONTIN.
CC	DR PROSITE: PS008B4; OSTEPONTIN; 1.
CC	KW Biominerization; Cell adhesion; Cytokine; Glycoprotein;
CC	KW Phosphorylation; Sialic acid; Signal.
FT	SIGNAL 1 22 Potential.
FT	CHAIN 23 317 Osteopontin.
FT	DOMAIN 86 96 Poly-Asp.
FT	SITE 144 146 Cell attachment site.
FT	CARBONYL 79 79 N-Linked (GlcNAc . . .) (Potential).
FT	CONFLICT 8 8 F -> L (In Ref. 2).
SQ	SEQUENCE 317 AA: 34963 MW: 73CB5C21FFF62310 CRC64;
Query	Query Match 33.3%; Score 111; DB 1; Length 317;
Best Local Similarity 64.5%; Pred. No. 0.0038;	
Matches 20; Conservative 4; Mismatches 7; Indels 0; Gaps 0;	
Qy	7 E V F T P V P V P T V D G R G D S V Y G R R S K S K K F 37
Db	129 D V L T P I A P T V D P D G R G D S L A Y G L R S K R S F 159
RESULT 14	
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ID	P97827;
AC	P97827;
DT	01-MAY-1997 (TRIMBLref. 03, Created)
DT	01-MAY-1997 (TRIMBLref. 03, Last sequence update)
DT	01-MAR-2004 (TRIMBLref. 26, Last annotation update)
DE	Osteopontin.
OS	Rattus norvegicus (Rat).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Search completed: July 27, 2005, 18:14:51
Job time : 173 sec₈